

STIC-Biotech/ChemLib

6:1994

From: Chen, Shin-Lin
Sent: Friday, March 08, 2002 4:01 PM
To: STIC-Biotech/ChemLib
Subject: interference search: 08/984,900

P

Please perform the following **sequence search for 08/984,900 ASAP**. Thanks!

Interference search for SEQ ID NO. 7 and 10.
Interference search for nucleotides 90-1203 of SEQ ID NO. 7.
Sequence search of SEQ ID No. 7 and 10 on issued patent data base.
Sequence search of nucleotides 90-1203 of SEQ ID No. 7 on issued patent data base.

12/14

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AU 1632
CM1 12A15
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Edward Han
Technical Info. Specialist
STIC/Biotech
PMI 6B02 Tel: 305-9203

	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher: _____	NA Sequences: <u>2</u>	STN: _____
Phone: _____	AA Sequences: <u>1</u>	DIALOG: _____
Location: _____	Structures: _____	Questel/Orbit: _____
Date Picked Up: <u>3/10/02</u>	Bibliographic: _____	DRLink: _____
Date Completed: <u>3/11/02</u>	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text: _____	Sequence Sys.: <u>12/14</u>
Clerical: _____	Patent Family: _____	WWW/Internet: _____
Online time: _____	Other: _____	Other (specify): _____

The first part of the document discusses the importance of maintaining accurate records of all transactions. It emphasizes that proper record-keeping is essential for the success of any business and for the protection of the interests of all parties involved. The document then goes on to describe the various methods and techniques used to collect and analyze data, and to provide a detailed account of the results of the study. The final part of the document discusses the implications of the findings and offers suggestions for further research.

Condore version 4.5
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ORF results: Protein sequence: us08-984-900-10

File: us08-984-900-10

Perfect score: 2015

Sequences: 2

Scoring table:

Gap: 10.0, Export: 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 98

Listing first 45 summaries

Database:

1: us08-984-900-10
2: us08-984-900-10
3: us08-984-900-10
4: us08-984-900-10
5: us08-984-900-10
6: us08-984-900-10

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCE

Result No.	Score	Match	Length	DB ID	Description
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2	1723.5	85.5	376	08-08-984-900-10	Sequence 2: Appl
3	1717.5	85.2	368	08-08-984-900-10	Sequence 3: Appl
4	1575	78.2	371	08-08-984-900-10	Sequence 4: Appl
5	1510	74.9	384	08-08-984-900-10	Sequence 5: Appl
6	1510	74.9	384	08-08-984-900-10	Sequence 6: Appl
7	1510	74.9	384	08-08-984-900-10	Sequence 7: Appl
8	1510	74.9	384	08-08-984-900-10	Sequence 8: Appl
9	1510	74.9	384	08-08-984-900-10	Sequence 9: Appl
10	1510	74.9	384	08-08-984-900-10	Sequence 10: Appl
11	1223	62.2	376	08-08-984-900-10	Sequence 11: Appl
12	642	41.9	376	08-08-984-900-10	Sequence 12: Appl
13	639	41.7	376	08-08-984-900-10	Sequence 13: Appl
14	638.5	41.7	376	08-08-984-900-10	Sequence 14: Appl
15	623	40.9	384	08-08-984-900-10	Sequence 15: Appl
16	622.5	40.9	384	08-08-984-900-10	Sequence 16: Appl
17	622.5	40.9	384	08-08-984-900-10	Sequence 17: Appl
18	622.5	40.9	384	08-08-984-900-10	Sequence 18: Appl
19	463	33.0	376	08-08-984-900-10	Sequence 19: Appl
20	279	13.0	154	08-08-984-900-10	Sequence 20: Appl
21	90.5	4.5	724	08-08-984-900-10	Sequence 21: Appl
22	90.5	4.5	724	08-08-984-900-10	Sequence 22: Appl
23	90.5	4.5	724	08-08-984-900-10	Sequence 23: Appl
24	90.5	4.5	724	08-08-984-900-10	Sequence 24: Appl
25	90.5	4.5	724	08-08-984-900-10	Sequence 25: Appl
26	87.5	4.3	339	08-08-984-900-10	Sequence 26: Appl
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28	86.5	4.3	311	08-08-984-900-10	Sequence 28: Appl
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33	86.5	4.3	339	08-08-984-900-10	Sequence 33: Appl
34	86.5	4.3	339	08-08-984-900-10	Sequence 34: Appl
35	86.5	4.3	339	08-08-984-900-10	Sequence 35: Appl
36	86.5	4.3	339	08-08-984-900-10	Sequence 36: Appl
37	86.5	4.3	339	08-08-984-900-10	Sequence 37: Appl
38	86.5	4.3	339	08-08-984-900-10	Sequence 38: Appl
39	86.5	4.3	339	08-08-984-900-10	Sequence 39: Appl
40	86.5	4.3	339	08-08-984-900-10	Sequence 40: Appl
41	86.5	4.3	339	08-08-984-900-10	Sequence 41: Appl
42	86.5	4.3	339	08-08-984-900-10	Sequence 42: Appl
43	86.5	4.3	339	08-08-984-900-10	Sequence 43: Appl
44	86.5	4.3	339	08-08-984-900-10	Sequence 44: Appl
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AL: COMMENTS

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Sequence 4: Appl
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Sequence 6: Appl
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Sequence 37: Appl
Sequence 38: Appl
Sequence 39: Appl
Sequence 40: Appl
Sequence 41: Appl
Sequence 42: Appl
Sequence 43: Appl
Sequence 44: Appl
Sequence 45: Appl

[illegible]

RESOL. 2
 DS-08-704 548 2
 : Sequence 2, Application DS/08704548
 : Date of Decision 07/07/08

APPLICANT: CALTECH, INC.
 APPLICANT: REFCO, PATENTIA M.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR VACCINING
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR VACCINING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STELLE, GEMMA, LAVERGNA & MENARDI, P. O.,
 STREET: SOTTO 1800, TWO PIONEER PLAZA
 CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZITE: 19102
 COMPUTER READABLE FORM:
 METHOD TYPE: PLATE, SLICK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pathologic Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/097,704, 519
 FILING DATE: 11 SEP 1996
 CLASSIFICATION: 4.24
 ATTORNEY/AGENT INFORMATION:
 NAME: MONTRO, DAVID A.
 REGISTRATION NUMBER: 30,460
 REFERENCE/SEQUENCE NUMBER: 9760 & 011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 564-8981
 TELEFAX: (215) 564-9549
 INFORMATION FOR SEQ. NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 topology: linear
 MOLECULE TYPE: protein
 OS: 08-704 546 2

Quarry Match	85.58	Score	1723.5	DB	2	Depth	376
Best Local Similarity	82.28	Prod. No.	1.28	172			
Matches	309	Conservative	44	Matches	28	Index	5
						Gaps	2

[illegible]

RESULTS

US-08-378-617A-11
; Sequence 11, Application US/08378617A

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Sequence 4, Application US/08042531

Patent No. 0200193

GENERAL INFORMATION:

APPLICANT: Lowe, John A.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

TITLE OF INVENTION: OF OLIGONUCLEOTIDE STRUCTURES ON OLIGONUCLEOTIDES,

TITLE OF INVENTION: OLIGONUCLEOTIDES, OR AS FREE MOLECULES, AND FOR THE ISOLATION

TITLE OF INVENTION: OF OLIGONUCLEOTIDE SEQUENCES THAT LOCATE TO THESE SEQUENCES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: JOHN A. LOWE, MOBILE, ALABAMA, 36688-0001

ADDRESSEE: P.O.

STREET: 1755 LITTLETON LANE HIGHWAY, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPILED: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent No. Release #1.0, Version #1.05

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08042531

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08042531

FILING DATE:

APPLICANT NUMBER: 08 08/220 441

FILING DATE: 30 MAR 1994

APPLICATION NUMBER: US 07/914,261

FILING DATE: 20 JUL 1992

ATTORNEY: 7 397 156 156 156

NAME: Lavalley, Jean Paul M. P.

REGISTRATION NUMBER: 41,451

TELEPHONE: (703) 521-4500

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TELEPHONE: (703) 521-4500

Query Match: 74.94, Score 1510, ID 4, Length 394,

Post Local Similarity: 72.78, Prod. No. 3.20-1503

Matches: 271, Conserved: 48, Mismatches: 48, Indels: 16, Gaps: 4

1. NAME: Lavalley, Jean Paul M. P.

REGISTRATION NUMBER: 41,451

TELEPHONE: (703) 521-4500

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1 APPLICANT: Hubert et al.
2 TITLE OF INVENTION: "44 Human secreted proteins
3 FILE REFERENCE: P202992
4 CURRENT APPLICANT'S NUMBER: 02715-050, 673
5 PRIORITY FILING DATE: 2002-01-18
6 PRIOR APPLICATION NUMBER: 60/264,240
7 PRIOR FILING DATE: 2001-01-24
8 PRIOR APPLICATION NUMBER: 60/264,681
9 PRIOR FILING DATE: 2001-01-24
10 PRIOR APPLICATION NUMBER: 60/264,125
11 PRIOR FILING DATE: 1999-12-14
12 PRIOR APPLICATION NUMBER: PCT/02/0474418
13 PRIOR FILING DATE: 1999-06-15
14 PRIOR APPLICATION NUMBER: 60/089,507
15 PRIOR FILING DATE: 1998-06-16
16 PRIOR APPLICATION NUMBER: 60/089,508
17 PRIOR FILING DATE: 1998-06-16
18 PRIOR APPLICATION NUMBER: 60/089,509
19 PRIOR FILING DATE: 1998-06-16
20 PRIOR APPLICATION NUMBER: 60/089,510
21 PRIOR FILING DATE: 1998-06-16
22 PRIOR APPLICATION NUMBER: 60/090,112
23 PRIOR FILING DATE: 1998-06-22
24 PRIOR APPLICATION NUMBER: 60/090,113
25 PRIOR FILING DATE: 1998-06-22
26 NUMBER OF SEQ ID NOS: 550
27 SOFTWARE: Patent In Vit. 2.0
28 SEQ ID NO 244
29 LENGTH: 90
30 TYPE: CDS
31 ORIGIN: Homo Sapiens
32 IN: 13 550 874-244

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? PRIOR FILING DATE: 1998-06-22
? PRIOR APPLICATION NUMBER: 60/7790, 114
? PRIOR FILING DATE: 1998-05-22
? NUMBER OF SEQ. ID NOS.: 510
? SOFTWARE: Patculta Ver. 2.0
? SEQ. ID NO. 421
? LENGTH: 90
? TYPE: FRT
? ORGANISM: Homo sapiens
Gen: 370-374-421

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Query Match	12.98	Score 259.57	18.6	100.00	90
Best Local Similarity	62.76	Prod. No. 5,496.17			
Matches	47	Conserved	157	Mismatches	12
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RESULT 14
DS-09-611-526-2754
SEQUENCE 2754, APPLICATION DS/00611526
GENERAL INFORMATION:
APPLICANT: OITA, TOSHIO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: ISOGAI, TAKAO
APPLICANT: HAYASHI, KOJI
APPLICANT: ISHII, SHIZUKO
APPLICANT: NAWATA, YUKI
APPLICANT: WAKAMATSU, AI
APPLICANT: FUJIMORI, MITSUO
APPLICANT: NAGAI, KEIICHI
APPLICANT: KASABA, SHINICHI
APPLICANT: GOSUKI, TETSUJI
APPLICANT: GOKA, HISASHI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIS OF FULL LENGTH CLONAS
TITLE OF INVENTION: AND THEIR USES
FILE REFERENCE: 03727012
CURRENT APPLICATION NUMBER: 2000-07-1745
CURRENT FILING DATE: 2000-07-07
PRIORITY APPLICATION NUMBER: JP 1999-194446
PRIORITY FILING DATE: 1999-07-08
PRIORITY APPLICATION NUMBER: JP 2000 18774
PRIORITY FILING DATE: 2000-01-11
PRIORITY APPLICATION NUMBER: JP 2000-18745
PRIORITY FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 484
SOFTWARE: PATENT IN VER. 2.1
CLASS: 35
LENGTH: 294
TYPE: PAT
ORGANISM: Homo sapiens
DS-09-611-526-2754

```

[illegible]

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[illegible]
$$K=U, \quad \psi=1$$
[illegible]

File: 15-08-984-900-7-0000-50-1000

Sequence:

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Figure 1

Maximum lbs Sec²

Post processing

Dalabasi :

fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being evaluated and is derived by analysis of the total score distribution.

5.1.1. MMARHS

[illegible]

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Query Match:	100.0%	Score 114:	DB 14:	Length 1269:
Best Local Alignment:	100.0%:	Prod No. 2:	as 364:	
Matched 114:	Conservation:	0:	Mismatches:	0:
			Indels:	0:
			Gaps:	0:

[illegible][illegible]

```

01 RESULT      3
02 US-09 598 816 7
03
04 ***RECORD OF REGISTRATION***
05
06 GENERAL INFORMATION:
07 APPLICANT: Clark Mr., John
08 SUBJECT: Domestic, Civil
09 TYPE OF AWARDING: Animal
10 FILE REFERENCE: 7407002
11
12 CLASSIFICATION NUMBER: 99-02-598,816
13 CURRENT FILING DATE: 2000-06-13
14 PRIORITY FILING DATE: 99-07-04,144
15 NUMBER OF SEQ ID NOS: 51
16 SOFTWARE: Patonlin Ver. 2.1
17 SEQ ID NO 7
18 LENGTH: 1269
19
20 TEXT: CNA
21 ORGANISM: Sus scrofa
22 FEATURED:
23 NAME/KEY: CDS
24 LOCATION: (16)..(111)
25 US-09-598-816-7

```

[illegible]

US 08 214 580 2
 1 Sequence 2 Application US/08214580
 2 GENERAL INFORMATION
 3 APPLICANT: Sandro M. Klee
 4 APPLICANT: Klee, Sandro M. Klee
 5 TITLE OF INVENTION: XENOTRANSPLANTATION
 6 NUMBER OF SEQUENCES: 4
 7 CORRESPONDENT ADDRESS:
 8 ADDRESS: Sandro M. Klee
 9 STREET: 1951 Buft Street
 10 CITY: Fairfield
 11 STATE: Connecticut
 12 COUNTRY: USA
 13 ZIP: 06430
 14 COMPUTER READABLE FORM:
 15 MODIFIER TYPE: 1.5, 1.6, 750 K, 25.7KHz
 16 COMPUTER: Intel 486/50
 17 OPERATING SYSTEM: DOS 5.2
 18 SOFTWARE: WordPerfect 6.0
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: US/08/214,580
 21 FILING DATE:
 22 CLASSIFICATION: 435
 23 PRIORITY INFORMATION:
 24 APPLICATION NUMBER: Australian Provisional
 25 FILING DATE: March 16, 1993
 26 ATTORNEY/AGENT: INTERMATTER
 27 NAME: Klee, Sandro M.
 28 REFERENCE/PRIOR NUMBER: 750 533
 29 TELEPHONE: (203) 255-1400
 30 TELEFAX: (203) 255-1101
 31 INFORMATION FOUR SEQ. ID NO.: 25
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 1423 base pairs
 34 TYPE: Multiple Acid
 35 STRANDEDNESS: Double
 36 TOPOLOGY: Linear
 37 MOLECULE TYPE: cDNA to mRNA
 38 DESCRIPTION: galactosyl transferase
 39 HYDROLYTIC ACT: No
 40 ANTISENSE: No
 41 ORIGIN: DIRECT
 42 ORGANISM: Sus scrofa
 43 US 08 214 580 2
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US 08 260 201 5
 1 Sequence 5 Application US/08260201
 2 GENERAL INFORMATION
 3 APPLICANT: Sandro M. Klee
 4 APPLICANT: Klee, Sandro M. Klee
 5 TITLE OF INVENTION: XENOTRANSPLANTATION
 6 NUMBER OF SEQUENCES: 5
 7 CORRESPONDENT ADDRESS:
 8 ADDRESS: Sandro M. Klee
 9 STREET: 1951 Buft Street
 10 CITY: Fairfield
 11 STATE: Connecticut
 12 COUNTRY: USA
 13 ZIP: 06430
 14 COMPUTER READABLE FORM:
 15 MODIFIER TYPE: 1.5, 1.6, 750 K, 25.7KHz
 16 COMPUTER: Intel 486/50
 17 OPERATING SYSTEM: DOS 5.2
 18 SOFTWARE: WordPerfect 6.0
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: US/08/260,201
 21 FILING DATE:
 22 CLASSIFICATION: 435
 23 PRIORITY INFORMATION:
 24 APPLICATION NUMBER: Australian Provisional
 25 FILING DATE: March 16, 1993
 26 ATTORNEY/AGENT: INTERMATTER
 27 NAME: Klee, Sandro M.
 28 REFERENCE/PRIOR NUMBER: 750 533
 29 TELEPHONE: (203) 255-1400
 30 TELEFAX: (203) 255-1101
 31 INFORMATION FOUR SEQ. ID NO.: 25
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 1423 base pairs
 34 TYPE: Multiple Acid
 35 STRANDEDNESS: Double
 36 TOPOLOGY: Linear
 37 MOLECULE TYPE: cDNA to mRNA
 38 DESCRIPTION: galactosyl transferase
 39 HYDROLYTIC ACT: No
 40 ANTISENSE: No
 41 ORIGIN: DIRECT
 42 ORGANISM: Sus scrofa
 43 US 08 260 201 5
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1 CLINICAL ID: 121
 2 ATTORNEY/AGENT INFORMATION:
 3 NAME: DAVID A. MULLIN
 4 REGISTRATION NUMBER: 40,480
 5 E-MAIL: dnmullin@att.net
 6 TELECOMMUNICATION INFORMATION:
 7 TELEPHONE: (215) 768-3333
 8 TELEFAX: (215) 568-5549
 9 INFORMATION FOR THE REPORT:
 10 SOURCE: CHAKA TESTS:
 11 LENGTH: 1141 base pairs
 12 TYPE: nucleic acid
 13 STRAND: sense
 14 TOPOLOGY: linear
 15 FEATURE:
 16 NAME: 9000
 17 LOCATION: 1,1143
 18 DB: 213 200A.1

Query Match: 74.1% Score: 870; DB: 6; Length: 1141;

Best Local Similarity: 87.1%; First No. Gap: 219; Matches: 984; Descriptive: 9; Mismatches: 140; Indels: 15; Gaps: 2;

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[illegible]

1 APPLICANT: Crawford, Robert J.
2 APPLICANT: Kuhn, John, Peter D.
3 TITLE OF INVENTION: MATERIALS AND METHOD FOR MANAGEMENT OF
4 TITLE OF INVENTION: HYPERACIDIC REJECTION IN HUMAN AND TRANSPLANTATION
5 NUMBER OF SEQUENCES: 33
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Fish & Richardson
8 STREET: 120 South Sixth Street, Suite 2500
9 CITY: Minneapolis
10 STATE: MN
11 COUNTRY: USA
12 ZIP: 55402
13 COMPUTER GENERATED FROM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC DOS/MS DOS
17 FILE NAME: 21000001.DAT
18 CURRENT APPLICATION DATA:
19 FILING DATE: 26 JAN 1995
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 NAME: MILLER, Mark S.
23 REGISTRATION NUMBER: 34,612
24 TELEPHONE: 612-339-9999
25 TELECOMMUNICATION INFORMATION:
26 FAX: 612-339-9999
27 TELEFAX: (612) 268 9606
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 4450 base pairs
31 TYPE: nucleic acid
32 ORGANISM: Simulium
33 ORGANISM: Simulium
34 SOURCE: ATCC
35

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APPLICANT: Sandrin, Mauro S.
APPLICANT: N-41
TITLE OF INVENTION: XENOTRANSPLANTATION
TITLE OF INVENTION: THERAPEUTIC
NUMBER OF SEQUENCES: 4
CORRESPONDING AUTHOR:
ADDRESS: Maurice M. Klee
STREET: 1961 Burr Street
CITY: Fairfield
STATE: CA 94503
COUNTRY: USA
ZIP: 94540
COMPUTER READABLE FORM:
METHOD: 111, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 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APPLICANT: Crawford, Robert J.
TITLE OF INVENTION: MATHEMATICAL METHOD FOR DETERMINING OF
NUMBER OF SEQUENCES: 43
CORRECTED NAME: Ashford
ADDRESS: Fish & Richardson
STREET: 120 South Sixth Street, Suite 2000
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER: PERMANENT
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC DOS 2.0
SOFTWARE: Fulltext Release #1.0, Version #1.008
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/03,617
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
AFFIRMED: 2, 15, 17, 19
NAME: Ellinger, Mark S.
REFERENCE: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 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2193, 2194, 2195, 2196, 2197, 2198, 2199, 220
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GenCore version 4.5
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OM nucleic acid search, using SW model

Run on: March 11, 2002, 10:56:00 : Search time 6373.65 seconds

(with 411 sequences)
510,755 Million cell alignments

Hit(s): US-08-984-900-7_copy_90_1203

Percent score:

Sequence:

Scoring table:

Database:

Total number of hits satisfying chosen parameters:

Minimum hit seq length:

Maximum hit seq length:

Post-processing:

Database:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being produced, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	871	78.2	1140	7	US-09-174-270-1	Sequence 1, April
2	716.4	64.3	1131	7	US-09-174-270-1	Sequence 1, April
3	660.4	59.3	1500	6	US-09-915-424-1	Sequence 1, April
4	660.4	59.3	1500	6	US-09-915-424-1	Sequence 1, April
5	185	16.6	1594	8	US-10-047-270-287	Sequence 2, April
6	177.4	15.6	1349	1	US-09-915-424-1	Sequence 1, April
7	176	15.8	1150	8	US-10-012-542-69	Sequence 69, April
8	176	15.8	1150	8	US-10-012-542-69	Sequence 69, April
9	174.6	15.6	1199	8	US-10-012-542-69	Sequence 69, April
10	174.6	15.6	1199	8	US-10-012-542-69	Sequence 69, April
11	165.8	14.9	388	6	US-09-915-424-1	Sequence 1, April
12	157.6	14.1	748	8	US-10-029-886-25488	Sequence 25, April
13	157.6	14.1	748	8	US-10-029-886-25488	Sequence 25, April
14	157.6	14.1	748	8	US-10-029-886-25488	Sequence 25, April
15	156.6	14.1	1926	7	US-09-915-424-1	Sequence 1, April
16	156.6	14.1	1926	7	US-09-915-424-1	Sequence 1, April
17	108.8	9.8	413	5	US-09-904-939-1159	Sequence 1159, April
18	94.2	6.4	442	6	US-09-915-424-1	Sequence 1, April
19	81.4	7.5	422	6	US-09-915-424-1	Sequence 1, April
20	57.4	5.2	470	7	US-09-915-424-1	Sequence 1, April
21	45.6	4.1	483	5	US-09-915-424-1	Sequence 1, April
22	41.4	3.7	508	6	US-09-915-424-1	Sequence 1, April
23	41.4	3.7	508	6	US-09-915-424-1	Sequence 1, April
24	41.4	3.7	508	6	US-09-915-424-1	Sequence 1, April

25	41.4	3.7	1416	7	US-09-174-270-1	Sequence 1, April
26	41.4	3.7	3017	5	US-09-614-150-10252	Sequence 10252, April
27	41.4	3.7	1080	5	US-09-614-150-10252	Sequence 10252, April
28	40	3.6	656	7	US-09-915-424-1	Sequence 1, April
29	39.8	3.6	450	7	US-09-915-424-1	Sequence 1, April
30	39.8	3.6	10779	7	US-09-915-424-1	Sequence 1, April
31	39.8	3.6	871	7	US-09-915-424-1	Sequence 1, April
32	39.2	3.5	516	7	US-09-614-150-10252	Sequence 10252, April
33	39.2	3.5	1504	5	US-09-614-150-10252	Sequence 10252, April
34	39.2	3.5	1504	5	US-09-614-150-10252	Sequence 10252, April
35	39.2	3.5	4501	5	US-09-614-150-10252	Sequence 10252, April
36	38.6	3.5	784	7	US-09-614-150-10252	Sequence 10252, April
37	38.6	3.5	784	7	US-09-614-150-10252	Sequence 10252, April
38	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
39	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
40	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
41	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
42	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
43	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
44	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April
45	38.6	3.5	2554	5	US-09-614-150-10252	Sequence 10252, April

ALGORITHMS

RESULT 1
US-09-174-270-1
Sequence 1, April
GENERAL INFORMATION:
Name: US-09-174-270-1
ID: 174-270-1
Description: US-09-174-270-1
Database: US-09-174-270-1
Scoring table: US-09-174-270-1
Total number of hits satisfying chosen parameters: 1
Minimum hit seq length: 1
Maximum hit seq length: 1
Post-processing: US-09-174-270-1
Database: US-09-174-270-1
Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being produced, and is derived by analysis of the total score distribution.

